IN THE SPECIFICATION

Please replace paragraph [0006] at page 2 with the following paragraph:

[0006] There are over 30 families of secondary transporters, also known as solute carriers or SLC (reviewed by Berger, *et al.* (2000) in *The Kidney: Physiology and Pathophysiology*, eds. Seldin DW and Giebisch G., Lippincott, Williams & Wilkins, Philadelphia 1:107-138; see also ~~www.gene.ucl.ac.uk/nomenclature~~ the website maintained by the HUGO gene nomenclature committee, University College London, UK). The SLC families are classified according to the pair of molecules they move. The SLC16 family transports monocarboxylate ions, coupled with the transport of protons.

Please replace paragraph [0024] at page 6 with the following paragraph:

[0024] Human 25466 contains the following regions or other structural features (for general information regarding PFAM identifiers, PS prefix and PF prefix domain identification numbers, refer to Sonnhammer *et al.* (1997) *Protein* 28:405-420 ~~and~~ ~~http://www.psc.edu/general/software/packages/pfam/pfam.html~~ or the Pfam website maintained in several locations, *e.g.* by the Sanger Institute (pfam.sanger.ac.uk), Washington University (pfam.wustl.edu), the Karolinska Institute (pfam.cgr.kr.se) or Institut de la National Recherche Agronomique (pfam.jouy.inra.fr)):

Please replace paragraph [0040] at page 9 with the following paragraph:

[0040] To identify the presence of an "MCT" domain in a 25466 protein sequence, and make the determination that a polypeptide or protein of interest has a particular profile, the amino acid sequence of the protein can be searched against the Pfam database of HMMs (*e.g.*, the Pfam database, release 2.1) using the default parameters (~~http://www.sanger.ac.uk/Software/Pfam/HMM_search~~ see the Pfam website maintained in several locations, *e.g.* by the Sanger Institute (pfam.sanger.ac.uk/Software/Pfam/HMM_search). For example, the hmmsf program, which is available as part of the HMMER package of search programs, is a family specific default program for MILPAT0063 and a score of 15 is the default threshold score for determining a hit. Alternatively, the threshold score for determining a hit can be lowered (*e.g.*, to 8 bits). A description of the Pfam database can be found in Sonhammer *et al.* (1997) *Proteins* 28:405-420 and a detailed description of HMMs can be found, for example, in Gribskov *et al.* (1990) *Meth. Enzymol.*183:146-159; Gribskov *et al.* (1987) *Proc. Natl. Acad.*

Sci. USA 84:4355-4358; Krogh *et al.* (1994) *J. Mol. Biol.* 235:1501-1531; and Stultz *et al.* (1993) *Protein Sci.* 2:305-314, the contents of which are incorporated herein by reference. A search was performed against the HMM database resulting in the identification of an "MCT domain" in the amino acid sequence of human 25466 at about residues 40 to 477 of SEQ ID NO:2.

Please replace paragraph [0077] at page 25 with the following paragraph:

[0077] The comparison of sequences and determination of percent identity between two sequences can be accomplished using a mathematical algorithm. In a preferred embodiment, the percent identity between two amino acid sequences is determined using the Needleman and Wunsch (1970) *J. Mol. Biol.* 48:444-453 algorithm which has been incorporated into the GAP program in the GCG software package (available at ~~http://www.geg.com~~ the bioinformatics page of the website maintained by Accelrys, Inc., San Diego, CA, USA), using either a Blossum 62 matrix or a PAM250 matrix, and a gap weight of 16, 14, 12, 10, 8, 6, or 4 and a length weight of 1, 2, 3, 4, 5, or 6. In yet another preferred embodiment, the percent identity between two nucleotide sequences is determined using the GAP program in the GCG software package ~~(available at http://www.geg.com)~~, using a NWSgapdna.CMP matrix and a gap weight of 40, 50, 60, 70, or 80 and a length weight of 1, 2, 3, 4, 5, or 6. A particularly preferred set of parameters (and the one that should be used if the practitioner is uncertain about what parameters should be applied to determine if a molecule is within a sequence identity or homology limitation of the invention) are a Blossum 62 scoring matrix with a gap penalty of 12, a gap extend penalty of 4, and a frameshift gap penalty of 5.

Please replace paragraph [0079] at page 25 with the following paragraph:

[0079] The nucleic acid and protein sequences described herein can be used as a "query sequence" to perform a search against public databases to, for example, identify other family members or related sequences. Such searches can be performed using the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to 25466 nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to 25466 protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described

in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25:3389-3402. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, XBLAST and NBLAST) can be used~~. See http://www.ncbi.nlm.nih.gov~~ (accessible at the website maintained by National Center for Biotechnology Information, Bethesda, MD, USA).

Please replace paragraph [00204] at page 55 with the following paragraph:

[00204] In another embodiment, determining the ability of the 25466 protein to bind to a target molecule can be accomplished using real-time Biomolecular Interaction Analysis (BIA) (see, *e.g.*, Sjolander, S. and Urbaniczky, C. (1991) *Anal. Chem.* 63:2338-2345 and Szabo *et al.* (1995) *Curr. Opin. Struct. Biol.* 5:699-705). "Surface plasmon resonance" or "BIA" detects biospecific interactions in real time, without labeling any of the interactants (*e.g.*, ~~BIAcore~~ BIACORE™). Changes in the mass at the binding surface (indicative of a binding event) result in alterations of the refractive index of light near the surface (the optical phenomenon of surface plasmon resonance (SPR)), resulting in a detectable signal which can be used as an indication of real-time reactions between biological molecules.

Please replace paragraph [00206] at page 55 with the following paragraph:

[00206] It may be desirable to immobilize either 25466, an anti-25466 antibody or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to a 25466 protein, or interaction of a 25466 protein with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided which adds a domain that allows one or both of the proteins to be bound to a matrix. For example, glutathione-S-transferase/25466 fusion proteins or glutathione-S-transferase/target fusion proteins can be adsorbed onto glutathione ~~sepharose~~ SEPHAROSE™ beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, which are then combined with the test compound or the test compound and either the non-adsorbed target protein or 25466 protein, and the mixture incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either

directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of 25466 binding or activity determined using standard techniques.

Please replace paragraph [00288] at page 76 with the following paragraph:

[00288] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, ~~Cremophor EL™~~ CREMOPHOR™ EL (BASF, Parsippany, NJ) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringability exists. It should be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyetheylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Please replace paragraphs [00367] and [00368] at page 98 with the following paragraphs:

[00367] Human 25466 expression was measured by ~~TaqMan®~~ TAQMAN™ quantitative PCR (Perkin Elmer Applied Biosystems) in cDNA prepared from a variety of normal and diseased (e.g., cancerous) human tissues or cell lines.

[00368] Probes were designed by PrimerExpress software (PE Biosystems) based on the sequence of the human 25466 gene. Each human 25466 gene probe was labeled using FAM (6-carboxyfluorescein), and the β2-microglobulin reference probe was labeled with a different fluorescent dye, VIC. The differential labeling of the target gene and internal reference gene

thus enabled measurement in same well. Forward and reverse primers and the probes for both β2-microglobulin and target gene were added to the ~~TaqMan®~~ TAQMAN™ Universal PCR Master Mix (PE Applied Biosystems). Although the final concentration of primer and probe could vary, each was internally consistent within a given experiment. A typical experiment contained 200nM of forward and reverse primers plus 100nM probe for β-2 microglobulin and 600 nM forward and reverse primers plus 200 nM probe for the target gene. ~~TaqMan~~ TAQMAN™ matrix experiments were carried out on an ABI PRISM™ 7700 Sequence Detection System (PE Applied Biosystems). The thermal cycler conditions were as follows: hold for 2 min at 50°C and 10 min at 95°C, followed by two-step PCR for 40 cycles of 95°C for 15 sec followed by 60°C for 1 min.

Please replace paragraph [00369] at page 98-99 with the following paragraph:

[00369] The following method was used to quantitatively calculate human 25466 gene expression in the various tissues relative to β-2 microglobulin expression in the same tissue. The threshold cycle (Ct) value is defined as the cycle at which a statistically significant increase in fluorescence is detected. A lower Ct value is indicative of a higher mRNA concentration. The Ct value of the human 25466 gene is normalized by subtracting the Ct value of the β-2 microglobulin gene to obtain a $_{\Delta}$Ct value using the following formula: $_{\Delta}Ct=Ct_{\text{human }\sout{59914 \text{ and } 59921}\ 25466} - Ct_{\beta\text{-2 microglobulin}}$. Expression is then calibrated against a cDNA sample showing a comparatively low level of expression of the human 25466 gene. The $_{\Delta}$Ct value for the calibrator sample is then subtracted from $_{\Delta}$Ct for each tissue sample according to the following formula: $_{\Delta\Delta}Ct=_{\Delta}Ct_{\text{-sample}} - {}_{\Delta}Ct_{\text{-calibrator}}$. Relative expression is then calculated using the arithmetic formula given by $2^{-\Delta\Delta Ct}$. Expression of the target human 25466 gene in each of the tissues tested is then graphically represented as discussed in more detail below.